Fig.1

A Mouse ST8Sia VI

```
CGGAGCGGCGAGTCGGTGCCGCCCGGGCTGCGCTTCGCCCCGGCAGCTTTGGCGGCGAGGACGCCCGTGGCTCAGGATGAGATCGGGGGGCACGCTGTTC    100
                                                                        M  R  S  G  G  T  L  F           8
GCCCTCATAGGCAGCCTGATGCTGCTGCTCCTCCTGCGTATGCTCTGGTGCCCAGCCGACGCGCCTGCCCGCTCCAGGCTGTTGATGGAGGGAAGCAGAG    200
A  L  I  G  S  L  M  L  L  L  L  L  R  M  L  W  C  P  A  D  A  P  A  R  S  R  L  L  M  E  G  S  R  E       42
AGGACACCAGTGGTACCTCAGCTGCACTGAAGACACTCTGGAGCCCGACAACCCCGGTACCACGCACCAGGAACAGCACATATCTGGATGAGAAGACAAC    300
 D  T  S  G  T  S  A  A  L  K  T  L  W  S  P  T  T  P  V  P  R  T  R  N  S  T  Y  L  D  E  K  T  T        75
CCAAATAACAGAGAAATGCAAAGATCTGCAATATAGCTTGAACTCTTTATCTAACAAAACGAGACGGTACTCTGAGGATGACTACCTCCAGACCATCACA    400
Q  I  T  E  K  C  K  D  L  Q  Y  S  L  N  S  L  S  N  K  T  R  R  Y  S  E  D  D  Y  L  Q  T  I  T        108
AACATACAGAGATGCCCATGGAACCGGCAAGCAGAAGAATATGACAATTTTAGAGCAAAACTGGCTTCCTGTTGCGATGCCATTCAAGACTTCGTGGTTT    500
N  I  Q  R  C  P  W  N  R  Q  A  E  E  Y  D  N  F  R  A  K  L  A  S  C  C  D  A  I  Q  D  F  V  V  S      142
CCCAGAACAACACTCCAGTGGGGACTAACATGAGCTACGAGGTGGAAAGCAAGAAACACATCCCCATTCGAGAGAACATTTTCCACATGTTTCCAGTGTC    600
Q  N  N  T  P  V  G  T  N  M  S  Y  E  V  E  S  K  K  H  I  P  I  R  E  N  I  F  H  M  F  P  V  S        175
GCAGCCTTTTGTGGACTATCCCTATAACCAGTGTGCAGTGGTTGGTAATGGGGGAATTCTCAACAAGTCTCTCTGCGGAGCAGAAATTGATAAATCTGAC    700
Q  P  F  V  D  Y  P  Y  N  Q  C  A  V  V  G  N  G  G  I  L  N  K  S  L  C  G  A  E  I  D  K  S  D       208
TTCGTCTTCAGGTGTAACCTCCCCCCAATCACAGGGAGCGCTAGTAAAGATGTTGGAAGCAAACAAATCTTGTGACTGTCAATCCCAGCATTATAACCC    800
F  V  F  R  C  N  L  P  P  I  T  G  S  A  S  K  D  V  G  S  K  T  N  L  V  T  V  N  P  S  I  I  T  L     242
TGAAGTACCAGAATTTGAAGGAGAAGAAAGCACAGTTTTTGGAGGACATCTCCACCTATGGAGATGCATTCCTCCTGCCAGCATTTTCTATCGGGC       900
K  Y  Q  N  L  K  E  K  K  A  Q  F  L  E  D  I  S  T  Y  G  D  A  F  L  L  P  A  F  S  Y  R  A          275
CAACACAGGCATCTCTTTTAAAGTCTACCAAACACTCAAAGAGTCAAAAATGAGGCAAAAGGTTCTCTTCTTCCATCCCAGGTACCTGAGACACCTCGCT    1000
N  T  G  I  S  P  K  V  Y  Q  T  L  K  E  S  K  M  R  Q  K  V  L  F  F  H  P  R  Y  L  R  H  L  A       308
CTTTTCTGGAGAACTAAAGGGGTGACTGCATACCGCTTGTCCACAGGCTTGATGATTGCAAGTGTCGCTGTGGAACTGTGTGAAAACGTGAAGCTCTACG    1100
L  F  W  R  T  K  G  V  T  A  Y  R  L  S  T  G  L  M  I  A  S  V  A  V  E  L  C  E  N  V  K  L  Y  G     342
GATTCTGGCCTTTCTCTAAGACTATCGAAGACACCCCACTCAGTCACCACTACTATGATAACATGTTACCTAAGCATGGTTTCCACCAGATGCCTAAAGA    1200
 F  W  P  F  S  K  T  I  E  D  T  P  L  S  H  H  Y  Y  D  N  M  L  P  K  H  G  F  H  Q  M  P  K  E      375
ATACAGCCAAATGCTCCAGCTCCATATGAGAGGAATCCTCAAACTGCAATTCAGCAAATGTGAAACGGCTTAACGTTTCTTAGAAGGAGAATAATTTCAG    1300
Y  S  Q  M  L  Q  L  H  M  R  G  I  L  K  L  Q  F  S  K  C  E  T  A  *                                  398
GAGGTGGAGTGGATGTGTCACAGCATCTCCAAAAAGCCAATAGAAGAAGGCACAGAGAAAGCATGAATTACAAAGGCGCTCTCCCACTTGTCTAGACCAA    1400
AGCCACCCGCCCCCACTCACTTTGCAGCCTCCACGAGTCACTCATTCTCACCTTCAACGTTCTTTCTCTGAGAATAGAGACCAAAACATCAGACTTGGAT    1500
```

B Human ST8Sia VI

```
GGTGGCGGCGGCGGCGGGAGCCGCGAGTCGGGGCCGCCCGGGCTGTGCTTCGCCCCGGCAGCAGCGGTGGCGGCGGCGCCTGTGGCTCAGGATGCGGCCG    100
                                                                           M  R  P                      3
GGGGGGCGCACTGCTCGCCCTGCTCGCCAGCCTGCTGCTGCTGCTGCTGCTGCCTGCTCTGGTGCCCGGCAGACGCGCCCGGCCGCGCCAGGATTCTGG    200
G  A  L  L  A  L  L  A  S  L  L  L  L  L  L  L  R  L  L  W  C  P  A  D  A  P  G  R  A  R  I  L  V         37
TGGAGGAAAGCAGGGAGGCCACCCACGGCACCCCCGCAGCGCTGAGGACGCTCCGGAGCCCGGCGACCGCGGTACCGCGCGCCACTAACAGCACATATCT    300
E  E  S  R  E  A  T  H  G  T  P  A  A  L  R  T  L  R  S  P  A  T  A  V  P  R  A  T  N  S  T  Y  L        70
GAATGAGAAGTCGCTCCAACTGACGGAGAAATGCAAAAATCTGCAATATGGCATTGAGTCTTTCTCTAACAAAACGAAAGGGTATTCAGAGAACGACTAC    400
N  E  K  S  L  Q  L  T  E  K  C  K  N  L  Q  Y  G  I  E  S  F  S  N  K  T  K  G  Y  S  E  N  D  Y       103
CTTCAGATTATCACAGATATACAGAGTTGTCCATGGAAACGGCAAGCAGAAGAATATGCAAATTTTAGAGCCAAACTTGCTTCCTGCTGTGATGCTGTTC    500
L  Q  I  I  T  D  I  Q  S  C  P  W  K  R  Q  A  E  E  Y  A  N  F  R  A  K  L  A  S  C  C  D  A  V  Q     137
AAAACTTTGTTGTTTCTCAGAATAACACTCCAGTTGGGACTAAATATGAGTTACGAGGTGGAAAGCAAAAAAGAAATCCCAATTAAGAAGAACATTTTCA    600
N  F  V  V  S  Q  N  N  T  P  V  G  T  N  M  S  Y  E  V  E  S  K  K  E  I  P  I  K  K  N  I  F  H        170
TATGTTTCCAGTGTCCCAGCCTTTTGTGGACTACCCTTATAATCAGTGTGCAGTGGTCGGAAATGGGGGAATTCTGAATAAGTCTCTCTGTGGAACTGAA    700
M  F  P  V  S  Q  P  F  V  D  Y  P  Y  N  Q  C  A  V  V  G  N  G  G  I  L  N  K  S  L  C  G  T  E       203
ATAGATAAATCCGACTTCGTTTTTAGGTGTAACCTACCCCCAACCACAGGAGATGTTAGTAAAGATGTTGGCAGTAAAACAAATCTTGTGACTATAAATC    800
I  D  K  S  D  F  V  F  R  C  N  L  P  P  T  T  G  D  V  S  K  D  V  G  S  K  T  N  L  V  T  I  N  P     237
CAAGCATCATAACTCTGAAATATGGGAACTTAAAGGAAAAAAAAGCCCTATTTTTGGAGGACATTGCAACCTATGGAGATGCATTTTTTTTTCTGCCAGC    900
 S  I  I  T  L  K  Y  G  N  L  K  E  K  K  A  L  F  L  E  D  I  A  T  Y  G  D  A  F  F  L  P  A         270
ATTTTCCTTCAGGGCCAACACGGGTACCTCTTTCAAAGTATACTACACGCTCGAAGAGTCTAAAGCAAGACAAAAGGTTCTATTTTTCCATCCCAAGTAC    1000
F  S  F  R  A  N  T  G  T  S  F  K  V  Y  Y  T  L  E  E  S  K  A  R  Q  K  V  L  F  F  H  P  K  Y       303
CTGAAAGATCTGGCCCTTTTCTGGAGAACTAAAGGTGTGACTGCATACCGCTTGTCCACCGGCTTGATGATCACAAGTGTTGCAGTGGAACTGTGTAAAA    1100
L  K  D  L  A  L  F  W  R  T  K  G  V  T  A  Y  R  L  S  T  G  L  M  I  T  S  V  A  V  E  L  C  K  N     337
ATGTGAAGCTGTATGGATTCTGGCCCTTCTCTAAAACTGTAGAAGACATACCTGTCAGCCATCACTATTATGACAACAAGCTACCTAAACATGGTTTCCA    1200
 V  K  L  Y  G  F  W  P  F  S  K  T  V  E  D  I  P  V  S  H  H  Y  Y  D  N  K  L  P  K  H  G  F  H      370
TCAGATGCCCAAAGAATAACGCAGATCCTCCAACTTCACATGAAAGGAATCCTCAAACTGCAATTTAGCAAATGTGAAGTCGCCTAAACAAAGTATCTT    1300
Q  M  P  K  E  Y  S  Q  I  L  H  M  K  G  I  L  K  L  Q  F  S  K  C  E  V  A  *                         398
AAAAATGGGAATAATTTTAATATAATGCAGTAGGTGATTAACAATGTCTCCAAACACCAAAGGAGGTGGCTAAAGAGTATTTTGAGATGAGCCCCAAAATT    1400
TGGTTTGACCAAAGCTTCCCCACTCATTTTGCAATGATGGCAAGTCATTCAATCCTTCTCATCTTCATTTTTTCTCCTTATAACATGGACACCATATCTG    1500
```
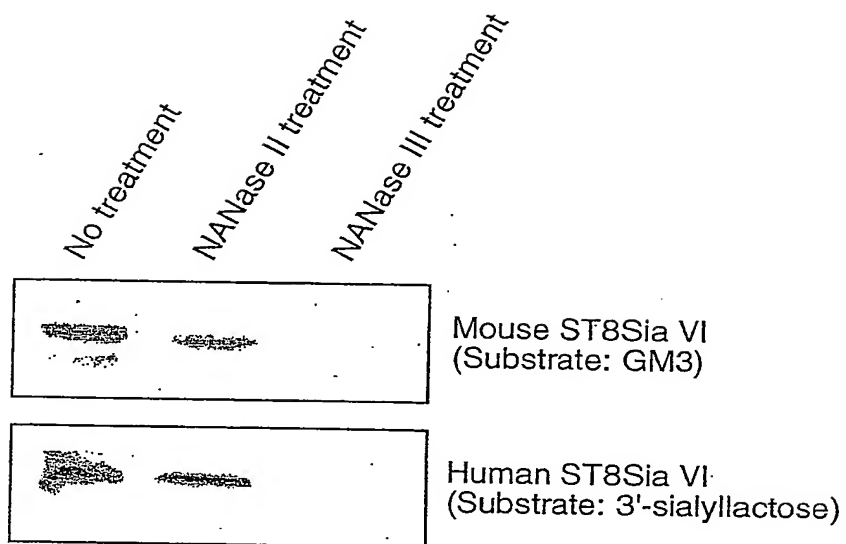
Fig.2

A

```
ST8Sia I    1   M--S-ECG-RAIHTSR---------G-AM-AMIAR----K-F-PF-T-RL--PVG---A--    31
ST8Sia V    1   MRYADESANRDILGNRTLLFIFICAFALVTLIQQILYSKSYIKF-GFQFGWQRGIQQANW     59
ST8Sia VI   1   -----------MRSGGTLFAILGSLMILLLIRMLWCPADAPAFSRLLMEGSRDITSGTS     48

ST8Sia I    32  SAI-----C-V---VV--LCWLY-IF--EV-Y---F-IPNEKEIVQG-VIA---CRT--A     66
ST8Sia V    60  TGIFNDSDSPTEQNITGSSSRMFEFYKPELEFNSTECIELRQEIIEVKVISMVKCSEIFE    119
ST8Sia VI   49  AAI-KTLWSPTTPVPRTRNSTYLD-EFTTQITEKCKDLQYSLNSISNKTRRYSEDDYI-Q    105

ST8Sia I    67  WRT-N--Q----TS-ASLFHRQMEDCCIPAHLEAMTKMNSFMGKSIWDGELLYSFTII    117
ST8Sia V    120 RWKSLCIDKWAMGASEASLFKSTISRCCNAPNFLFTTCKNTPVETNIRYEVESSGLYHII    179
ST8Sia VI   106 TITNICRCFWNRQAEEYDNFRAKLASCCDAIQDEVVSQNNTPVGTNMSYEVESKKHIPIR    165

ST8Sia I    118 NSTYSLFHQATE-FQLELKKCAVVGNGGILKMSGCARQIDEPNFVMRCNLPFLGSEYTRI    176
ST8Sia V    180 QEIFKMFFKEMEYYRSQFKKCAVVGNGGILKNSGCKEINSADFVMRCNLPPISGIYITI    239
ST8Sia VI   166 ENIHHMFFVSQFVDYFYNQCAVVGNGGILNKSICCAEIDKSDFVFRCNLPPITGSASKI    225

ST8Sia I    177 VGSKTQLVTANPSIIRQRFENI-LWSRKKFVDNMKIYNHSYIYMPAFSMKTGIEPSLRVY    235
ST8Sia V    240 VGEKTDVVTVNPSIIIDRFHKIEKW-RRPFFSVLQRYENASVLLPAFYNVRNILVSFRVK    298
ST8Sia VI   226 VGSKTNLVTVNPSIITLKYQNLKE-KKAQFLEDISTYGDAFLLLPAFSYRANTGISFKVY    284

ST8Sia I    236 YTLKIVGANCTVLFANFLFNIGKFWKSRGIHAKRLSTGIFLVSAALGLCEEVSIYGFW    295
ST8Sia V    299 MMIDDFQSRQPVYFFHHQYISSVSRYWLSLGVRARHISTGISLVTAALELCEEVHIFGFW    358
ST8Sia VI   285 QTLKESKMRQKVLFFHERYLFHLALFWRTKGVTAYRLSTGIMIASVAVELCENVKLYGFW    344

ST8Sia I    296 PFSVNMQGDPISHHYYDNVLFSGYHAMFEFLQLWYLFKIGALRMGLDPCEEPSPQPTS    355
ST8Sia V    359 AFPMNPSGFFITHHYYDNVKPKPGFHAMFSEIFTFIRMHSRGILRVHTGTC-NCC-----   412
ST8Sia VI   345 PFSKTIEDTELSHHYYDNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA------   398
```
                                           *   *

B

```
mST8Sia VI   1   MRSGGTLFAILGSIMLLLLLFMLWCPADAPAFSRLLMEGSRDISGTSAALKTLWSPTTP    60
hST8Sia VI   1   MRPGGALLAILLASIILLLLLFILWCPADAFGFAHILVESREAIHGTPAALRTIRSPAIA    60

mST8Sia VI   61  VPHTRNSTYLDEKTTGITEKCRDLQYSLNSLSNKTRRYSEDDYLCIITNICRCPWNRQAE    120
hST8Sia VI   61  VPHATNSTYINEKSLGLTEKCKNLQYGIESFSNKTKGYSENDYLCIITDICSCPWKRQAE    120

mST8Sia VI   121 EYDNFRAKLASCCDAIQDFVVSQNNTPVGTNMSYEVESKKHIPIRENIFHMFPVSQPFVI    180
hST8Sia VI   121 EYANFRAKLASCCDAVQNFVVSQNNTPVGTNMSYEVESKKPIPIKKNIFHMFPVSQPFVI    180

mST8Sia VI   181 YPYNQCAVVGNGGILNKSLCCAEIDKSDFVFRCNLPFITGSASKDVGSKTNLVTVNPSII    240
hST8Sia VI   181 YPYNQCAVVGNGGILNKSLCGTEIDKSDFVFRCNLPFTTGDVSKDVGSKTNLVTINPSII    240

mST8Sia VI   241 TLKYQNLKEKKAQFLEDISTYGDAFLLLPAFSYRANTGISFKVYQTIKESKMRQKVLFFH    300
hST8Sia VI   241 TLKYGNLKEKKALFLEDIATYGDAFFFLPAFSFRANTGTSFKVYYTIEESKARQKVLFFH    300

mST8Sia VI   301 ERYIRHLALFWRTKGVTAYRLSTGLMIASVAVELCENVKLYGFWPFSKTIEITELSHHYY    360
hST8Sia VI   301 EKYIKDLALFWRTKGVTAYRLSTGLMITSVAVELCKNVKLYGFWPFSKTVEDIEVSHHYY    360

mST8Sia VI   361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA                        398
hST8Sia VI   361 DNKLPKHGFHQMPKEYSQILQLHMKGILKLQFSKCEVA                        398
```

Fig.3

A

No treatment   NANase II treatment   NANase III treatment

Mouse ST8Sia VI
(Substrate: GM3)

Human ST8Sia VI
(Substrate: 3'-sialyllactose)

B

1	2	3
GD3	GM3	Product

Mouse ST8Sia VI

Fig.4

Mouse ST8Sia III | Mouse ST8Sia VI | Human ST8Sia VI

− + − + − +

N-Glycanase treatment

4/12

Fig.5

A

GD3   GQ1b   COS-7   COS-7+
ST8Sia VI

1   2   3   4

- GD3

- GT1a

- GQ1b

B

COS-7
COS-7+ST8Sia VI
COS-7
COS-7+ST8Sia VI

MW   −   −   +   +   *N*-Glycanase
(kDa)   1   2   3   4   treatment

208 —
119 —
94.0 —

51.1 —

35.4 —

28.8 —

Fig.6

A

Mouse
ST8Sia VI

Actin

B

Fig.7

A

Human ST6Gal II

```
ggcgccgggactccctcctggccgcccacagcctgtgcgcattcctgcattcctgccgccgcccgggacccgagcccccggaggtgtccaggcgcggtgc      100

caggcgggtactgtgcaggttcattctgccacccatctgcattaagacacaaggtgctgaccgcagagacctgccatgaaaccacacttgaagcaatgga      200
                                                                    M  K  P  H  L  K  Q  W  R        9

gacaacgaatgcttttcggaatattcgcttggggggctcctcttttttgctgattttcatctacttcaccgacagcaacccccgctgagcctgtacccagctc  300
 Q  R  M  L  F  G  I  F  A  W  G  L  L  F  L  L  I  F  I  Y  F  T  D  S  N  P  A  E  P  V  P  S  S       42

cctctccttcctggagaccaggaggctcctgccggtgcaggggaagcagcgggccatcatgggcgccgcacatgagcccctccccgcctggggggcctggac    400
 L  S  F  L  E  T  R  R  L  L  P  V  Q  G  K  Q  R  A  I  M  G  A  A  H  E  P  S  P  P  G  G  L  D       75

gcacgccaggcgctgccccgcgcccacccagccggttcctttcatgcggggcctggagacctgcagaaatgggcccagtcccaagatgggtttgaacata     500
 A  R  Q  A  L  P  R  A  H  P  A  G  S  F  H  A  G  P  G  D  L  Q  K  W  A  Q  S  Q  D  G  F  E  H  K     109

aagagtttttttcatcccaggtgggggagaaaatctcaaagtgctttctacccgaggatgacgactacttttttgctgctggtcagccagggtggcacag     600
 E  F  F  S  S  Q  V  G  R  K  S  Q  S  A  F  Y  P  E  D  D  D  Y  F  F  A  A  G  Q  P  G  W  H  S       142

ccacactcaggggacattgggattcccttccccgggagccaggcccagaggaggggcttttccggctgcacaggtccagaggaggcgggtgaagaag       700
 H  T  Q  G  T  L  G  F  P  S  P  G  E  P  G  P  R  E  G  A  F  P  A  A  Q  V  Q  R  R  R  V  K  K       175

aggcaccggaggcagagaaggagccacgtgttggaggagggcgacgacggcgacaggctgtactcctccatgtccaggcttcctgtaccggctctgga     800
 R  H  R  R  Q  R  R  S  H  V  L  E  E  G  D  D  G  D  R  L  Y  S  S  M  S  R  A  F  L  Y  R  L  W  K     209

agggggaacgtctcttccaaaatgctgaacccgcgcctgcagaaggcgatgaaggattacctgaccgccaacaagcacggggtgcgcttccgcgggaagcg    900
 G  N  V  S  S  K  M  L  N  P  R  L  Q  K  A  M  K  D  Y  L  T  A  N  K  H  G  V  R  F  R  G  K  R       242

ggaggccgggctgagcagggcacagctgctgtgccagctgcggagccgcgcgcgcgtgcggacgctggacggcaccgaggcgcccttttctgcgctgggc    1000
 E  A  G  L  S  R  A  Q  L  L  C  Q  L  R  S  R  A  R  V  R  T  L  D  G  T  E  A  P  F  S  A  L  G       275

tggcggcgcctggtgcccgtgcccctgagccagctgcaccccgcggcctgcgcagctgcgctgtcgtcatgtctgcaggcgcaatcctcaactctt       1100
 W  R  R  L  V  P  A  V  P  L  S  Q  L  H  P  R  G  L  R  S  C  A  V  V  M  S  A  G  A  I  L  N  S  S     309

ccttgggcgaggaaatagattctcatgatgccggttttgagattaactctgctcctcacacgtggttatgagaaagatgttgggaataaaaccaccatacg   1200
 L  G  E  E  I  D  S  H  D  A  V  L  R  F  N  S  A  P  T  R  G  Y  E  K  D  V  G  N  K  T  T  I  R       342

catcattaattcgcagattctgaccaacccccagccatcacttcattgacagttcactgtataaagacgtcattttggtggcctgggaccctgccccatat   1300
 I  I  N  S  Q  I  L  T  N  P  S  H  H  F  I  D  S  S  L  Y  K  D  V  I  L  V  A  W  D  P  A  P  Y       375

tccgcaaatcttaacctgtggtacaaaaaaccggattacaacctgttcactccatatattcagcatcgtcagagaaacccaaatcagccattttacattc    1400
 S  A  N  L  N  L  W  Y  K  K  P  D  Y  N  L  F  T  P  Y  I  Q  H  R  Q  R  N  P  N  Q  P  P  F  Y  I  L  409

ttcatcctaaatttatatggcagctctgggatattatccaggagaacactaaagagaagattcaaccaaacccaccatcttctggtttcattggaatcct    1500
 H  P  K  P  I  W  Q  L  W  D  I  I  Q  E  N  T  K  E  K  I  Q  P  N  P  P  S  S  G  F  I  G  I  L       442

catcatgatgtccatgtgcagagaggtgcacgtgtatgaatatatcccatccgtgcggcagacggagctgtgccactaccacgagctgtactacgacgca   1600
 I  M  M  S  M  C  R  E  V  H  V  Y  E  Y  I  P  S  V  R  Q  T  E  L  C  H  Y  H  E  L  Y  Y  D  A       475

gcctgcaccctcggggcgtaccacccactactctatgagaagctcctggtgcagcgcctgaacatgggcacgcaggggatttgcatcgcaagggcagg     1700
 A  C  T  L  G  A  Y [H] P  L  L  Y [E] K  L  L  V  Q  R  L  N  M  G  T  Q  G  D  L  H  R  K  G  K  V     509

tggttcttcctggcttccaggcgtgcactgcctgccaccaagtccagtcattccacactcttaaaaaggggtttcttgggaatcaatgtgcaataaggta    1800
 V  L  P  G  F  Q  A  V  H  C  P  A  P  S  P  V  I  P  H  S  *                                          529
```

Short form

```
ttcatcctaaatttatatggcagctctgggatattatccaggagaacactaaagagaagattcaaccaaacccaccatcttctggtttcattggctcatt    1500
 H  P  K  P  I  W  Q  L  W  D  I  I  Q  E  N  T  K  E  K  I  Q  P  N  P  P  S  S  G  F  I  G  S  F       442

tgtaaaaattggccatatcagagcttgcagtgagccgagatcacgcgactgcactccagcctggacgacagagtgagactccatctcaaaaaaaaaaaa    1600
 V  K  I  G  H  I  R  A  C  S  E  P  R  S  R  D  C  T  P  A  W  T  T  E  *                              466
```
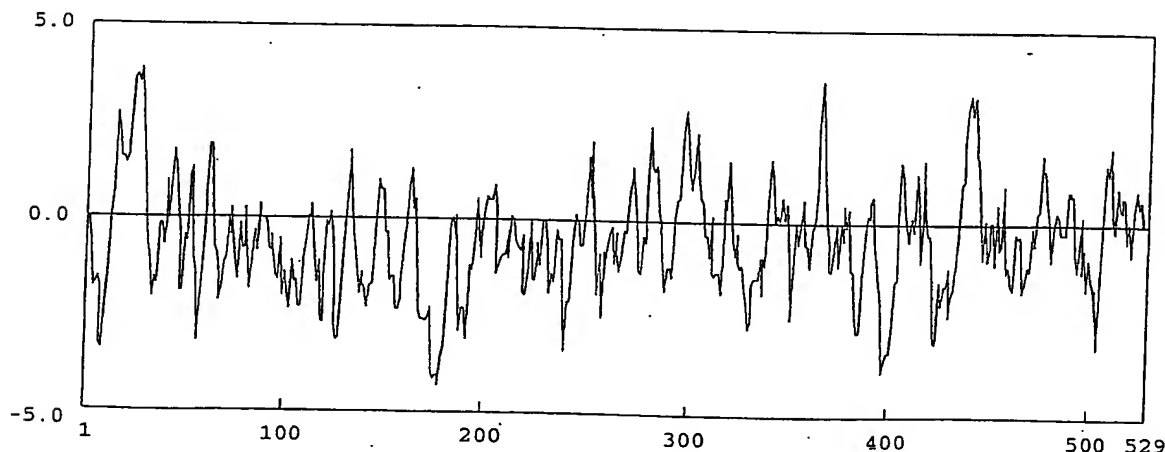
B

Hydropathy plot with y-axis from −5.0 to 5.0 (0.0 midline) and x-axis residue positions 1, 100, 200, 300, 400, 500, 529.

7/12

Fig.8

A

Mouse ST6Gal II

```
CAATGAAACCACACTTGAAGCAATGGCGACAACGAATGCTCTTTGGAATATTTGTTTGGGGGCTCCTCTTTTTGGCAATTTTCATCTACTTCACCAACAG      100
  M  K  P  H  L  K  Q  W  R  Q  R  M  L  F  G  I  F  V  W  G  L  L  L  F  L  A  I  F  I  Y  F  T  N  S       33

CAATCCTGCGGCACCTATGCCCAGCTCCTTTTTCCTTCCTGGAGAGCCGTGGGCTCCTGCCTCTACAGGGCAAGCAGCGGGTCATCATGGGCGCTTTGCAG      200
  N  P  A  A  P  M  P  S  S  F  S  F  L  E  S  R  G  L  L  P  L  Q  G  K  Q  R  V  I  M  G  A  L  Q          66

GAACCCTCTTTGCCCAGAAGTTTGGATGCAAGCAAAGTGCTTCTGGACAGCCACCCTGAGAACCCTTTCCACCCTTGGCCTGGGGACCCACAGAAATGGG       300
  E  P  S  L  P  R  S  L  D  A  S  K  V  L  L  D  S  H  P  E  N  P  F  H  P  W  P  G  D  P  Q  K  W  D      100

ATCAGGCCCCAAATGGCTTTGACAATGGGGATGAGTTTTTTTACATCCCAGGTTGGGAGGAAATCACAAAGCGCTTTCTATCCCGAGGAAGATAGCTATTT      400
  Q  A  P  N  G  F  D  N  G  D  E  F  F  T  S  Q  V  G  R  K  S  Q  S  A  F  Y  P  E  E  D  S  Y  F         133

TTTTGTTGCGGATCAGCCTGAGTTGTACCACCACAGGCAGGGTGCACTGGAGCTGCCATCTCCAGGGGAGACATCATGGCGATCAGGACCTGTTCAGCCC       500
  F  V  A  D  Q  P  E  L  Y  H  H  R  Q  G  A  L  E  L  P  S  P  G  E  T  S  W  R  S  G  P  V  Q  P        166

AAGCAGAAGCTGCTTCACCCAAGGCGAGGCAGCCTTGCCTGAGGAAGCCTATGACAGCGACATGCTGTCAGCCTCCATGTCGAGAGCCTTCCTGTACCGGC      600
  K  Q  K  L  L  H  P  R  R  G  S  L  P  E  E  A  Y  D  S  D  M  L  S  A  S  M  S  R  A  P  L  Y  R  L     200

TCTGGAAGGGGGCCGTGTCCTCTAAGATGTTGAACCCGCGCCTGCAGAAGGCCATGCGTTACTACATGTCCTTCAACAAGCATGGTGTGCGCTTCCGCAG      700
  W  K  G  A  V  S  S  K  M  L  N  P  R  L  Q  K  A  M  R  Y  Y  M  S  F  N  K  H  G  V  R  F  R  R        233

GCGGGGTCGGCGTGAAGCTACACGTACAGGGCCGGAGCTGCTGTGTGAGATGCGCAGACGTGTGCGTGTGCGCACGTTGGACGGCAGAGAGGCGCCCTTC      800
  R  G  R  R  E  A  T  R  T  G  P  E  L  L  C  E  M  R  R  R  V  R  V  R  T  L  D  G  R  E  A  P  F       266

TCGGGGCTGGGCTGGCGGCCTCTGGTACCAGGTGTACCTCTGAGCCAGTTGCACCCGCGCGGTCTGAGCAGCTGCGCAGTTGTCATGTCTGCCGGTGCCA      900
  S  G  L  G  W  R  P  L  V  P  G  V  P  L  S  Q  L  H  P  R  G  L  S  S  C  A  V  V  M  S  A  G  A  I     300

TCCTGAACTCCTCCTTGGGGGAGGAAATCGATTCTCATGATGCAGTTTTGAGATTTAACTCTGCCCCTACCCGTGGCTACGAGAAAGATGTCGGAAATAA      1000
  L  N  S  S  L  G  E  E  I  D  S  H  D  A  V  L  R  F  N  S  A  P  T  R  G  Y  E  K  D  V  G  N  K        333.

AACCACAGTACGCATCATTAATTCTCAGATTCTGGCCAACCCCAGCCATCACTTCATTGACAGTGCTTTATATAAAGATGTTATCCTGGTAGCCTGGGAT      1100
  T  T  V  R  I  I  N  S  Q  I  L  A  N  P  S  H  H  F  I  D  S  A  L  Y  K  D  V  I  L  V  A  W  D        366

CCTGCTCCTTATTCTGCCAATCTTAACCTGTGGTATAAGAAGCCAGATTACAACCTTTTCACTCCATATATCCAGCATCGCCGGAAATACCCGACTCAGC      1200
  P  A  P  Y  S  A  N  L  N  L  W  Y  K  K  P  D  Y  N  L  F  T  P  Y  I  Q  H  R  R  K  Y  P  T  Q  P     400

CATTTTACATTCTTCACCCCAAGTTCATATGGCAGCTTTGGGACATTATCCAGGAGAATACAAGGGAGAAGATACAGCCCAACCCACCATCTTCTGGTTT      1300
  F  Y  I  L  H  P  K  F  I  W  Q  L  W  D  I  I  Q  E  N  T  R  E  K  I  Q  P  N  P  P  S  S  G  F       433

TATTGGAATCCTCATCATGATGTCCATGTGTAAAGAGGTGCACGTGTATGAGTACATCCCATCTGTTCGACAGACAGAGCTTTGCCACTACCATGAGCTG      1400
  I  G  I  L  I  M  M  S  M  C  K  E  V  H  V  Y  E  Y  I  P  S  V  R  Q  T  E  L  C  H  Y  H  E  L       466

TACTACGACGCAGCCTGCACCTTGGGGGCCTACCACCCACTGCTCTATGAAAAGCTACTGGTGCAGCGCCCTTAACACAGGCACCCAGGCAGACTTGCATC      1500
  Y  Y  D  A  A  C  T  L  G  A  Y  H  P  L  L  Y  E  K  L  L  V  Q  R  L  N  T  G  T  Q  A  D  L  H  H     500

ACAAGGGCAAGGTAGTCTTGCCAGGCTTCCAGACCCTTCGGTGTCCAGTAACCAGCCCCAACAATACACATTCTTAAAATGGAACTCTTGGGAACTGATG      1600
  K  G  K  V  V  L  P  G  F  Q  T  L  R  C  P  V  T  S  P  N  N  T  H  S  *                               524

TGCAATAAGGT                                                                                               1611
```
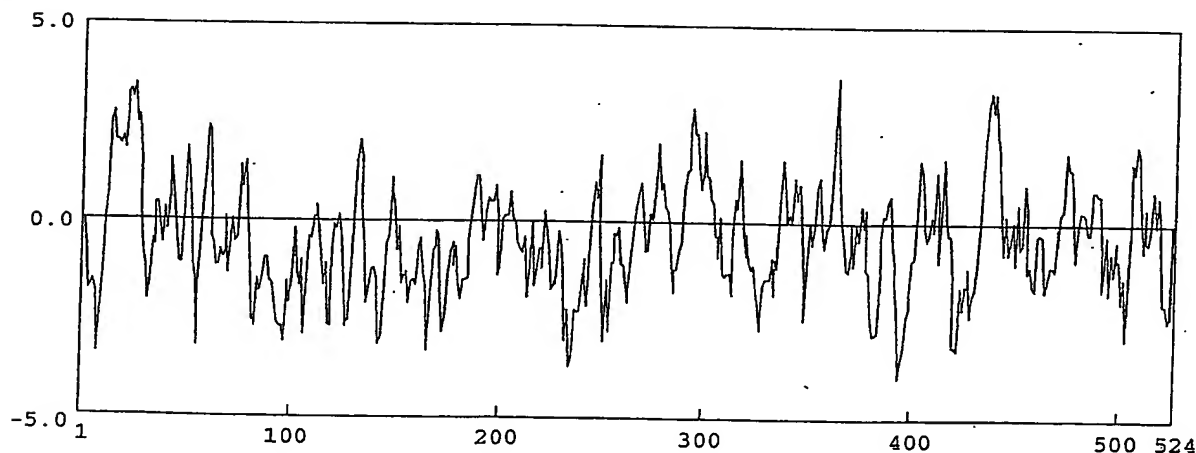
B

Fig.9

A

```
ST6Gal I      1  M-IH-TNLKKKFSCCVLVF-LLFAVICV-WKEKKKG-SYYDSFK-LQTKEFQVLKSLGKL    54
ST6Gal II     1  MKPHLKQWRQRMLFGIFAWGLLELLIFIYFTDSNPAEPVPSSLSFLEDRRLLPVQGKQRA    60

ST6Gal I     55  AMGSDSQSVSSSSTQDPHRGRQTLGSLRGLAKAKPEAS----------------------    92
ST6Gal II    61  IMGAAHEPSPPGGLDARQALPRAHPAGSFHBGPGDLQKWAQSQDGFEHKEFFSSQVGRKS   120

ST6Gal I     93  ------------------------------------------------------------    92
ST6Gal II   121  QSAFYPEDDDYFFAAGQPGWHSHTQGTLGFPSPGEPGPREGAFPAAQVQRRRVKKRHRRQ   180

ST6Gal I     93  ------------------------FQVWNKDSSSKNLIPRLQKIWKNYLSMNKYKMSYKB   128
ST6Gal II   181  RRSHVLEEGDDGDRLYSSMSRAFLYRLWKGNVSSKMLNPRLQKAMKDYITANKHGMRFRG   240

ST6Gal I    129  PGPGIKFSAEALRCHLRDHVNMSMVEVTDFPFNTSEWEGYLRKESIRTKAGPWG--RCAV   186
ST6Gal II   241  K-REAGLSRAQLLCQLRSRARVRTLDGTEAPFSALGWRRLVBAVPL-SQLHBRGLRSCAV   298

ST6Gal I    187  MSSAGSLKSSQLGREIDDHDAVLRFNGAPTANFQQDVGTKTTIRLMNSCLVT-TEKRFLK   245
ST6Gal II   299  MMSAGAILNSSLGEEIDSHDAVLRFNSAPTRGYEKDVGNKTTIRIINSCILDNPSHHFID   358

ST6Gal I    246  DSLYNEGILIVWDFSVVHSDIPKWYQNPDYNFFNNYKTYRKLHPNQPFYILKFQMPWELW   305
ST6Gal II   359  SSLYKDVILVAWDEAPYSANLNLWYKKPDYNLFTPMIQHRQRNPNQPFYILHEKFIWQLW   418

ST6Gal I    306  DILQEISPBEIQPNPPSSGMLGIIIMMTLDDQMDIVEFLPSKRKIDVCYMYQKFFDSACT   365
ST6Gal II   419  DTIDENTKEKIQPNPPSSGFIGILIMMSMQREMHVYEYIPSVRQTELQHYHELYYDAACT   478

ST6Gal I    366  MGAYHPLLYEKNLVKHLNQGTDEDIYLLGKATLPGFRTIHC                    406
ST6Gal II   479  LGAYHPLLYEKLLVQRLNMGTQGDLHRKGKVVLPGFQAVHCPAPSPVIPHS          529
                     *        *
```

B

```
hST6Gal II     1  MKPHLKQWRQRMLFGIFAWGLLFLLIFIYFTDSNPAEPVPSSLSFLETRRLLPVQGKQRA    60
mST6Gal II     1  MKPHLKQWRQRMLFGIFVWGLLFLAIFIYFTNSNPAAPMPSSFSFLESRGLLPLQGKQRV    60

hST6Gal II    61  IMGAAHEPSPPGGLDARQALPRAHPAGSFHAGPGDLQKWAQSQDGFEH-KEFFSSQVGRK   119
mST6Gal II    61  IMGALQEPSLPRSLDASKVLLDSHPENPFHPWPGDPQKWDQAPNGFDNGDEFFTSQVGRK   120

hST6Gal II   120  SQSAFYPEDDDYFFAAGQPGWHSHTQGTLGFPSPGEPGPREGAFPAAQVQRRRVKKRHRR   179
mST6Gal II   121  SQSAFYPEEDSYFFVADQPELYHHRQGALELPSPGETSWRSG--H---VQPKQ-KLLH--   172

hST6Gal II   180  QRRSHVLEEGDDGDRLYSSMSRAFLYRLWKGNVSSKMLNPRLQKAMKDMLTANKHGVRF-   238
mST6Gal II   173  PRRGSLPEEAYESDMLSASMSRAFLYRLWKGAVSSKMLNPRLQKAMRYMSFNKHGVRFR   232

hST6Gal II   239  -RGKREAGLSRAQLLCQLRSRARVRTLDGTEAPFSALGWRRLVHAVPLSQLHPRGLRSCA   297
mST6Gal II   233  RRGRREATRTGPELLCEMRRRVRVRTLDGREAPFSGLGWRPLVFGVPLSQLHPRGLSSCA   292

hST6Gal II   298  VVMSAGAILNSSLGEEIDSHDAVLRFNSAPTRGYEKDVGNKTTIRIINSQILTNPSHHFI   357
mST6Gal II   293  VVMSAGAILNSSLGEEIDSHDAVLRFNSAPTRGYEKDVGNKTTVRIINSQILANPSHHFI   352

hST6Gal II   358  DSSLYKDVILVAWDPAPYSANLNLWYKKPDYNLFTPYIQHRQRNPNQPFYILHPKFIWQL   417
mST6Gal II   353  DSALYKDVILVAWDPAPYSANLNLWYKKPDYNLFTPYIQHRRKYFTQPFYILHPKFIWQL   412

hST6Gal II   418  WDIIQENTKEKIQPNPPSSGFIGILIMMSMQREVHVYEYIPSVRQTELCHYHELYYDAAQ   477
mST6Gal II   413  WDIIQENTREKIQPNPPSSGFIGILIMMSMCKEVHVYEYIPSVRQTELCHYHELYYDAAQ   472

hST6Gal II   478  TLGAYHPLLYEKLLVQRLNMGTQGDLHRKGKVVLPGFQAVHCPAPSPVIPHS          529
mST6Gal II   473  TLGAYHPLLYEKLLVQRLNTGTQADLHHKGKVVLPGFQTLRCFVTSPNNTHS          524
```
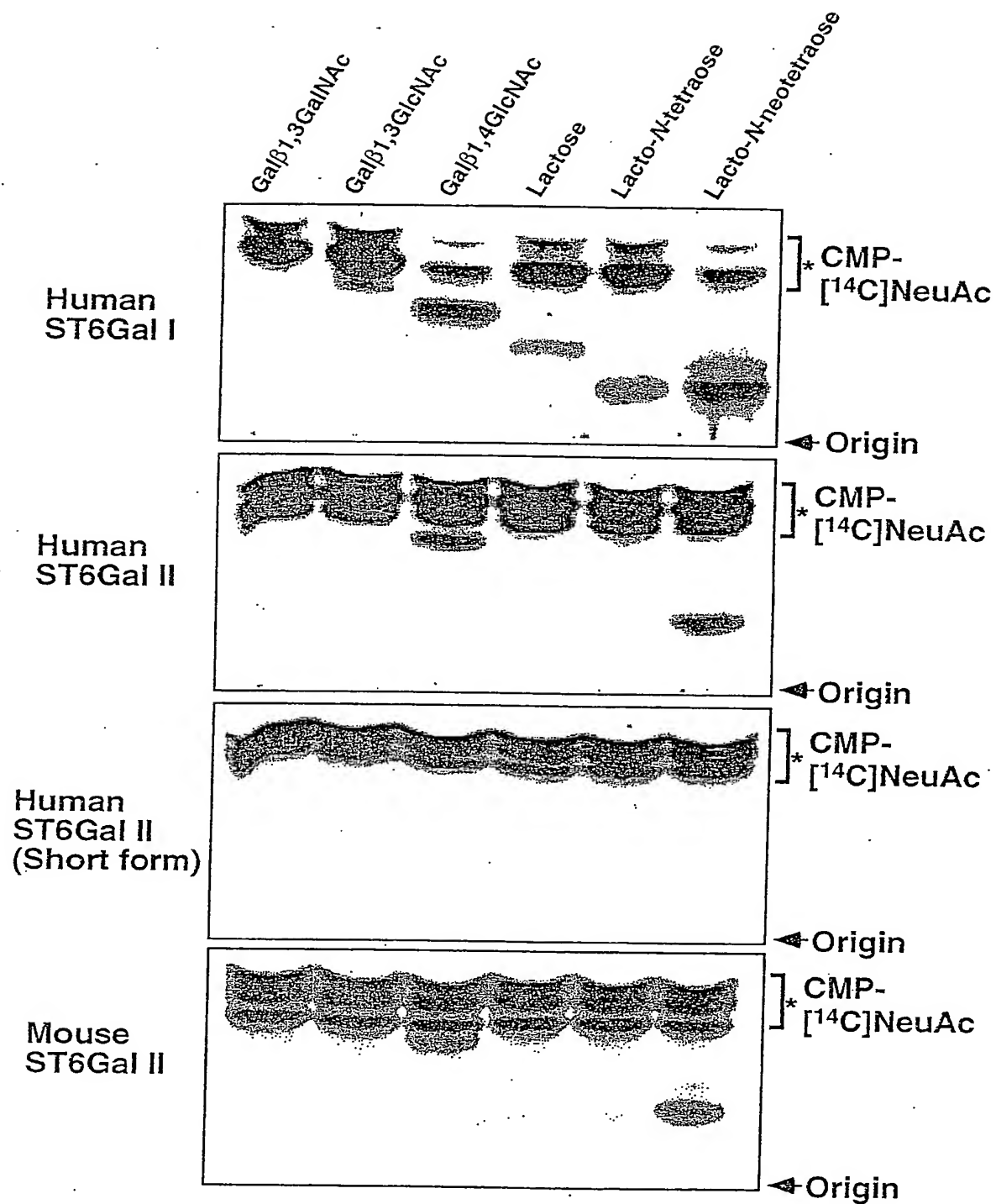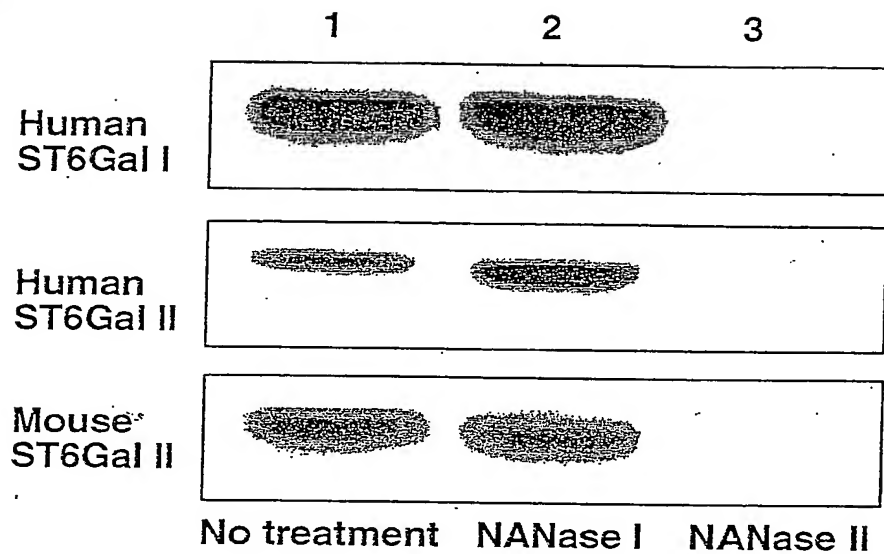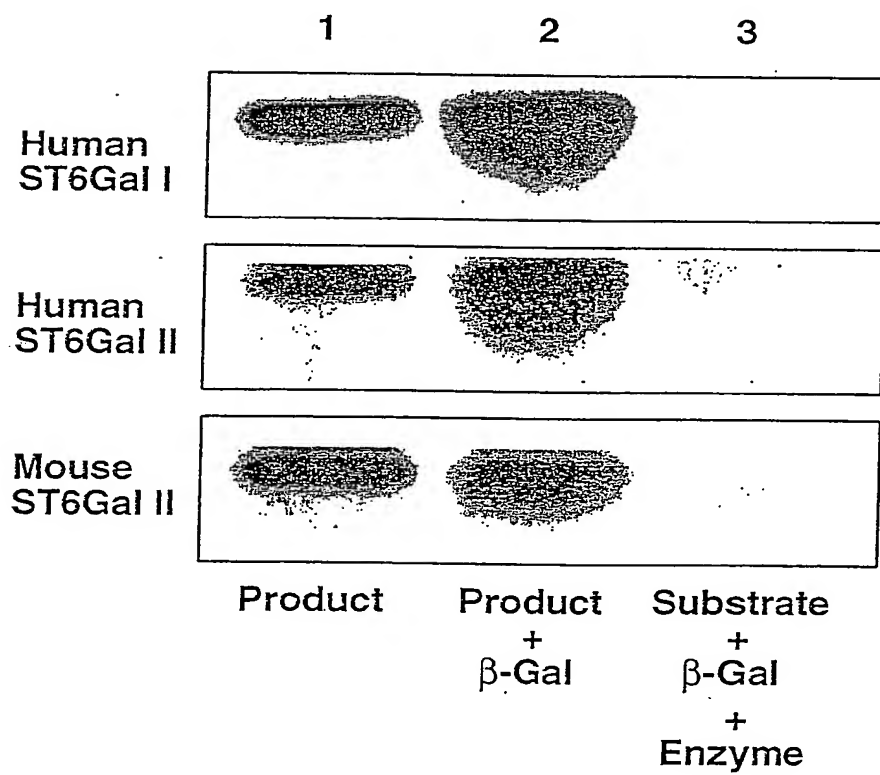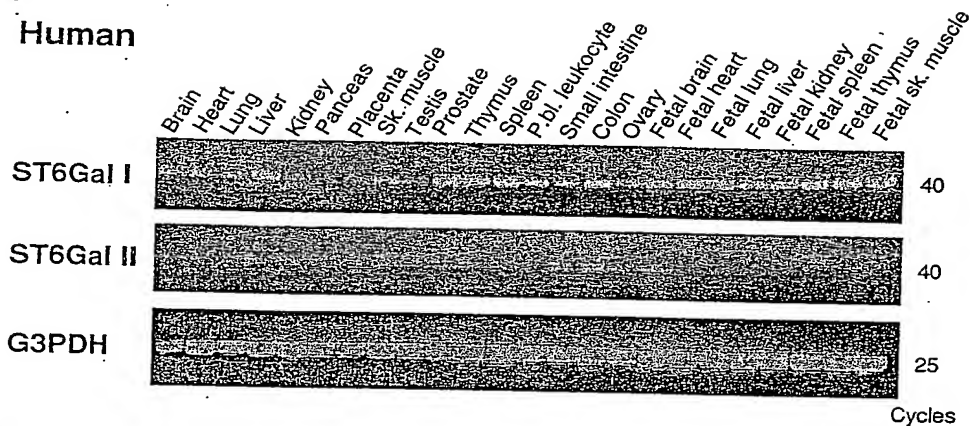
Fig.10

Fig.11

A

B

Fig.12

A

Human

ST6Gal I ... 40

ST6Gal II ... 40

G3PDH ... 25

Cycles

Brain, Heart, Lung, Liver, Kidney, Panceas, Placenta, Sk. muscle, Testis, Prostate, Thymus, Spleen, P.bl. leukocyte, Small intestine, Colon, Ovary, Fetal brain, Fetal heart, Fetal lung, Fetal liver, Fetal kidney, Fetal spleen, Fetal thymus, Fetal sk. muscle

B

Human

Breast carcinoma GI-101, Ovarian carcinoma GI-102, Pancreatic adenocarcinoma GI-103, Prostatic adenocarcinoma PC3, Lung carcinoma LX-1, Lung carcinoma GI-117, Colon adenocarcinoma CX-1, Colon adenocarcinoma GI-112

ST6Gal I ... 40

ST6Gal II ... 40

G3PDH ... 25

Cycles

C

Mouse

Heart, Brain, Spleen, Lung, Liver, Sk. muscle, Kidney, Testis, 7-day Embryo, 11-day Embryo, 15-day Embryo, 17-day Embryo

ST6Gal II ... 40

G3PDH ... 25

Cycles